SEQUENCE LISTING

<110> Kossida, Sophia

<120> Regulation of Ceramide Kinase

<130> 004974.00951

<150> US 09/969,896
<151> 2001-10-04

<150> US 60/238,005
<151> 2000-10-06

<150> US 60/314,113
<151> 2001-08-23

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 979
<212> DNA
<213> Homo sapiens

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taacaaattc tatgttaact atgtagaagt aattactgaa catgctaatc aggccaagga 180
gactctgtat gagattaaca tagacaaata cgacggcatc gtctgtgtcg gcggagatgg 240
tatgttcagc gaggtgctgc acggtctgat tgggaggacg cagaggagcg ccggggtcga 300
ccagaaccac ccccgggctg tgctggtccc cagtagcctc cggattggaa tcattcccgc 360
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gctgcatatc gttgttgggg actcgctggc catggatgtg tcctcagtcc accacaacag 480
cacactcctt cgctactccg tgtccctgct gggctacggc ttctacgggg acatcatcaa 540
ggacagtgag aagaaacggt ggttgggtct tgccagatac gacttttcag gtttaaagac 600
cttcctctcc caccactgct atgaagggac agtgtccttc ctccctgcac aacacacggt 660
gggatctcca agggatagga agccctgccg ggcaggatgc tttgtttgca ggcaaagcaa 720
gcagcagctg gaggaggagc agaagaaagc actgtatggt ttggaagctg cggaggacgt 780
ggaggagtgg caagtcgtct gtgggaagtt tctggccatc aatgccacaa acatgtcctg 840
tgcttgtcgc cggagcccca ggggcctctc cccggctgcc cacttgggag acgggtcttc 900
tgacctcatc ctcatccgga aatgctccag gttcaatttt ctgagatttc tcatcaggca 960
caccaaccag caggaccag 979

<210> 2
<211> 326
<212> PRT
<213> Homo sapiens

<400> 2
Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly Gly Lys Gly Gln
 1   5   10   15
Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu Phe Thr Leu Ala
            20   25   30
Ser Ile Thr Thr Asp Ile Ile Gly Asn Lys Phe Tyr Val Asn Tyr Val
        35   40   45
Glu Val Ile Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu
    50   55   60
Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly
65   70   75   80
Met Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser
                85   90   95
Ala Gly Val Asp Gln Asn His Pro Arg Ala Val Leu Val Pro Ser Ser
            100   105   110
Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp Cys Val Cys Tyr
        115   120   125
Ser Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala Leu His Ile Val
    130   135   140
Val Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val His His Asn Ser
145   150   155   160
Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr Gly Phe Tyr Gly
                165   170   175
Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu Gly Leu Ala Arg
            180   185   190
Tyr Asp Phe Ser Gly Leu Lys Thr Phe Leu Ser His His Cys Tyr Glu
        195   200   205
Gly Thr Val Ser Phe Leu Pro Ala Gln His Thr Val Gly Ser Pro Arg
    210   215   220
Asp Arg Lys Pro Cys Arg Ala Gly Cys Phe Val Cys Arg Gln Ser Lys
225   230   235   240
Gln Gln Leu Glu Glu Glu Gln Lys Lys Ala Leu Tyr Gly Leu Glu Ala
                245   250   255
Ala Glu Asp Val Glu Glu Trp Gln Val Val Cys Gly Lys Phe Leu Ala
            260   265   270
Ile Asn Ala Thr Asn Met Ser Cys Ala Cys Arg Arg Ser Pro Arg Gly
        275   280   285
Leu Ser Pro Ala Ala His Leu Gly Asp Gly Ser Ser Asp Leu Ile Leu
    290   295   300
Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu Ile Arg His
305   310   315   320
Thr Asn Gln Gln Asp Gln
                325

<210> 3
<211> 638
<212> PRT
<213> Homo sapiens

<400> 3

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            20                  25                  30
Leu Thr Ser Gln Ala Leu His Ile Gln Arg Leu Arg Pro Phe Thr Lys
        35                  40                  45
Pro Glu Ala Arg Pro Arg Gly Gly Leu Val Pro Leu Ala Glu Val Ser
    50                  55                  60
Gly Cys Cys Thr Leu Arg Ser Arg Ser Pro Ser Asp Ser Ala Ala Tyr
65                  70                  75                  80
Phe Cys Ile Tyr Thr Tyr Pro Arg Gly Arg Arg Gly Ala Arg Arg Arg
                85                  90                  95
Ala Thr Arg Thr Phe Arg Ala Asp Gly Ala Phe Thr Ala Thr Tyr Glu
            100                 105                 110
Glu Asn Arg Ala Glu Ala Gln Arg Trp Ala Thr Ala Leu Thr Cys Leu
        115                 120                 125
Leu Arg Gly Leu Pro Leu Pro Gly Asp Gly Glu Ile Thr Pro Asp Leu
    130                 135                 140
Leu Pro Arg Pro Pro Arg Leu Leu Leu Leu Val Asn Pro Phe Gly Gly
145                 150                 155                 160
Arg Gly Leu Ala Trp Gln Trp Phe Thr Cys Lys Asn His Val Leu Pro
                165                 170                 175
Met Ile Ser Glu Ala Gly Leu Ser Phe Asn Leu Ile Gln Thr Glu Arg
            180                 185                 190
Gln Asn His Ala Arg Glu Leu Val Gln Gly Leu Ser Leu Ser Glu Trp
        195                 200                 205
Asp Gly Ile Val Thr Val Ser Gly Asp Gly Leu Leu His Glu Val Leu
    210                 215                 220
Asn Gly Leu Leu Phe Thr Asp Arg Pro Asp Trp Glu Glu Ala Val Lys
225                 230                 235                 240
Met Pro Val Gly Ile Leu Pro Cys Gly Ser Gly Asn Ala Leu Ala Gly
                245                 250                 255
Ala Val Asn Gln His Gly Gly Phe Glu Pro Ala Leu Gly Leu Asp Leu
            260                 265                 270
Leu Leu Asn Cys Ser Leu Leu Leu Cys Arg Gly Gly Gly His Pro Leu
        275                 280                 285
Asp Phe Thr Leu Leu Ser Val Thr Leu Ala Ser Gly Ser Arg Cys Phe
    290                 295                 300
Ser Phe Leu Ser Val Ala Trp Gly Phe Val Ser Asp Val Asp Ile Gln
305                 310                 315                 320
Ser Glu Arg Phe Arg Ala Leu Gly Ser Ala Arg Phe Thr Leu Gly Thr
                325                 330                 335
Val Leu Gly Leu Ala Thr Leu His Thr Tyr Arg Gly Arg Leu Phe Thr
            340                 345                 350
Ser Tyr Leu Pro Ala Thr Val Glu Pro Ala Ser Pro Thr Pro Ala His
        355                 360                 365
Ser Leu Pro Arg Ala Lys Ser Glu Leu Thr Leu Thr Pro Asp Pro Ala
    370                 375                 380
Pro Pro Met Ala His Ser Pro Leu His Arg Ser Val Ser Asp Leu Pro
385                 390                 395                 400
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Leu Pro Leu Pro Gln Pro Ala Leu Ala Ser Pro Phe Thr Gly Ser Pro
                405                 410                 415
Glu Pro Leu Pro Ile Leu Ser Leu Asn Gly Gly Gly Pro Glu Leu Ala
            420                 425                 430
Gly Asp Trp Gly Gly Ala Gly Asp Ala Pro Leu Ser Pro Asp Pro Leu
        435                 440                 445
Leu Ser Ser Pro Pro Gly Ser Pro Lys Ala Ala Leu His Ser Pro Val
    450                 455                 460
Ser Glu Gly Ala Pro Val Ile Pro Phe Thr Pro Ser Ser Gly Leu Pro
465                 470                 475                 480
Leu Pro Thr Pro Asp Ala Arg Val Gly Ala Ser Thr Cys Gly Pro Pro
                485                 490                 495
Asp His Leu Leu Pro Pro Leu Gly Thr Pro Leu Pro Pro Asp Trp Val
            500                 505                 510
Thr Leu Glu Gly Asp Phe Val Leu Met Leu Ala Ile Ser Pro Ser His
        515                 520                 525
Leu Gly Ala Asp Leu Phe Thr Val Ala Ala Pro His Ala Arg Phe Asp
    530                 535                 540
Asp Gly Leu Val His Leu Cys Trp Val Arg Ser Gly Ile Ser Arg Ala
545                 550                 555                 560
Ala Leu Leu Arg Leu Phe Leu Ala Met Glu Arg Gly Ser His Phe Ser
                565                 570                 575
Leu Gly Cys Pro Gln Leu Gly Tyr Ala Ala Ala Arg Ala Phe Arg Leu
            580                 585                 590
Glu Pro Phe Thr Leu Thr Pro Arg Gly Val Leu Thr Val Asp Gly Glu
        595                 600                 605
Gln Val Glu Tyr Gly Pro Leu Gln Ala Gln Met His Pro Gly Ile Gly
    610                 615                 620
Thr Leu Leu Thr Gly Pro Pro Gly Cys Pro Gly Arg Glu Pro
625                 630                 635
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<210> 4
<211> 474
<212> DNA
<213> Homo sapiens

<400> 4
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cggggtcgac cagaaccacc cccgggctgt gctggtcccc agtagcctcc ggattggaat 120
cattcccgca gggtcaacgg actgcgtgtg ttactccacc gtgggcacca gcgacgcaga 180
aacctcggcg ctgcatatcg ttgttgggga ctcgctggcc atggatgtgt cctcagtcca 240
ccacaacagc acactccttc gctactccgt gtccctgctg ggctacggct tctacgggga 300
catcatcaag gacagtgaga agaaacggtg gttgggtctt gccagatacg acttttcagg 360
tttaaagacc ttcctctccc accactgcta tgaagggaca gtgtccttcc tccctgcaca 420
acacacggtg ggatctccaa gggataggaa gccctgccgg gcaagatgct ttgg 474

<210> 5
<211> 329
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(329)
<223> n = A,T,C or G

<400> 5
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ttaacataga caaatacgac ggcatcgtct gtgtcggcgg agatggtatg ttcagcgagg 120
tgctgcacgg tctgattggg aggacgcaga ggagcgccgg ggtcgaccag aaccaccccc 180
gggctgtgct ggtccccagt agcctccgga ttggaatcat tcccgcaggt caaacggact 240
gcgtgtntta ctccaccgtg ggcancagcg acgcagaaac ctcggcgctg catatcgttg 300
ttggggactc gctggccatg gatgtgtcc 329

<210> 6
<211> 167
<212> DNA
<213> Homo sapiens

<400> 6
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aacacacggt gggatctcca agggatagga agccctgccg ggcaggatgc tttgtttgca 120
ggcaaagcaa gcagcagctg gaggaggagc agaagaaagc actgtat 167

<210> 7
<211> 153
<212> DNA
<213> Homo sapiens

<400> 7
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ccgtgtccct gctgggctac ggcttctacg gggacatcat caaggacagt gagaagaaac 120
ggtggttggg tcttgccaga tacgactttt cag 153

<210> 8
<211> 550
<212> DNA
<213> Homo sapiens

<400> 8
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agcccggcgg cggagatggg ggcgacgggg gcggcggagc cgctgcaatc cgtgctgtgg 120
gtgaagcagc agcgctgcgc cgtgagcctg gagcccgcgc gggctctgct gcgctggtgg 180
cggagcccgg ggcccggagc cggcgccccc ggcgcggatg cctgctctgt gcctgtatct 240
gagatcatcg ccgttgagga aacagacgtt cacgggaaac atcaaggcag tggaaaatgg 300
cagaaaatgg aaaagcctta cgcttttaca gttcactgtg taaagagagc acgacggcac 360
cgctggaagt gggcgcaggt gactttctgg tgtccagagg agcagctgtg tcacttgtgg 420
ctgcagaccc tgcgggagat gctggagaag ctgacgtcca gaccaaagca tttactggta 480
tttatcaacc cgtttggagg aaaaggacaa ggcaagcgga tatatgaaag aaaagtggca 540
ccactgttca 550

<210> 9
<211> 1614
<212> DNA
<213> Homo sapiens

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ggagccggcg cccccggcgc ggatgcctgc tctgtgcctg tatctgagat catcgccgtt 180
gaggaaacag acgttcacgg gaaacatcaa ggcagtggaa aatggcagaa aatggaaaag 240
ccttacgctt ttacagttca ctgtgtaaag agagcacgac ggcaccgctg gaagtgggcg 300
caggtgactt tctggtgtcc agaggagcag ctgtgtcact tgtggctgca gaccctgcgg 360
gagatgctgg agaagctgac gtccagacca aagcatttac tggtatttat caacccgttt 420
ggaggaaaag gacaaggcaa gcggatatat gaaagaaaag tggcaccact gttcacctta 480
gcctccatca ccactgacat catcgttact gaacatgcta atcaggccaa ggagactctg 540
tatgagatta acatagacaa atacgacggc atcgtctgtg tcggcggaga tggtatgttc 600
agcgaggtgc tgcacggtct gattgggagg acgcagagga gcgccggggt cgaccagaac 660
caccccgggg ctgtgctggt ccccagtagc ctccggattg gaatcattcc cgcagggtca 720
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atcgttgttg gggactcgct ggccatggat gtgtcctcag tccaccacaa cagcacactc 840
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gagaagaaac ggtggttggg tcttgccaga tacgactttt caggtttaaa gaccttcctc 960
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tgcgacgggg aggtcctgca cagccctgcc atcgaggtca gagtccactg ccagctggtt 1560
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<210> 10
<211> 537
<212> PRT
<213> Homo sapiens

<400> 10
Met Gly Ala Thr Gly Ala Ala Glu Pro Leu Gln Ser Val Leu Trp Val
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Lys Gln Gln Arg Cys Ala Val Ser Leu Glu Pro Ala Arg Ala Leu Leu
            20   25   30
Arg Trp Trp Arg Ser Pro Gly Pro Gly Ala Gly Ala Pro Gly Ala Asp
        35   40   45
Ala Cys Ser Val Pro Val Ser Glu Ile Ile Ala Val Glu Glu Thr Asp
    50   55   60
Val His Gly Lys His Gln Gly Ser Gly Lys Trp Gln Lys Met Glu Lys

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65                  70                  75                  80
Pro Tyr Ala Phe Thr Val His Cys Val Lys Arg Ala Arg Arg His Arg
                85                  90                  95
Trp Lys Trp Ala Gln Val Thr Phe Trp Cys Pro Glu Glu Gln Leu Cys
            100                 105                 110
His Leu Trp Leu Gln Thr Leu Arg Glu Met Leu Glu Lys Leu Thr Ser
        115                 120                 125
Arg Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly Gly Lys Gly
    130                 135                 140
Gln Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu Phe Thr Leu
145                 150                 155                 160
Ala Ser Ile Thr Thr Asp Ile Ile Val Thr Glu His Ala Asn Gln Ala
                165                 170                 175
Lys Glu Thr Leu Tyr Glu Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val
            180                 185                 190
Cys Val Gly Gly Asp Gly Met Phe Ser Glu Val Leu His Gly Leu Ile
        195                 200                 205
Gly Arg Thr Gln Arg Ser Ala Gly Val Asp Gln Asn His Pro Arg Ala
    210                 215                 220
Val Leu Val Pro Ser Ser Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser
225                 230                 235                 240
Thr Asp Cys Val Cys Tyr Ser Thr Val Gly Thr Ser Asp Ala Glu Thr
                245                 250                 255
Ser Ala Leu His Ile Val Val Gly Asp Ser Leu Ala Met Asp Val Ser
            260                 265                 270
Ser Val His His Asn Ser Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu
        275                 280                 285
Gly Tyr Gly Phe Tyr Gly Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg
    290                 295                 300
Trp Leu Gly Leu Ala Arg Tyr Asp Phe Ser Gly Leu Lys Thr Phe Leu
305                 310                 315                 320
Ser His His Cys Tyr Glu Gly Thr Val Ser Phe Leu Pro Ala Gln His
                325                 330                 335
Thr Val Gly Ser Pro Arg Asp Arg Lys Pro Cys Arg Ala Gly Cys Phe
            340                 345                 350
Val Cys Arg Gln Ser Lys Gln Gln Leu Glu Glu Glu Gln Lys Lys Ala
        355                 360                 365
Leu Tyr Gly Leu Glu Ala Ala Glu Asp Val Glu Glu Trp Gln Val Val
    370                 375                 380
Cys Gly Lys Phe Leu Ala Ile Asn Ala Thr Asn Met Ser Cys Ala Cys
385                 390                 395                 400
Arg Arg Ser Pro Arg Gly Leu Ser Pro Ala Ala His Leu Gly Asp Gly
                405                 410                 415
Ser Ser Asp Leu Ile Leu Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu
            420                 425                 430
Arg Phe Leu Ile Arg His Thr Asn Gln Gln Asp Gln Phe Asp Phe Thr
        435                 440                 445
Phe Val Glu Val Tyr Arg Val Lys Lys Phe Gln Phe Thr Ser Lys His
    450                 455                 460
Met Glu Asp Glu Asp Ser Asp Leu Lys Glu Gly Gly Lys Lys Arg Phe
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465                 470                 475                 480
Gly His Ile Cys Ser Ser His Pro Ser Cys Cys Cys Thr Val Ser Asn
                485                 490                 495
Ser Ser Trp Asn Cys Asp Gly Glu Val Leu His Ser Pro Ala Ile Glu
            500                 505                 510
Val Arg Val His Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu
        515                 520                 525
Glu Asn Pro Lys Pro Asp Ser His Ser
    530                 535
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<210> 11
<211> 562
<212> PRT
<213> Homo sapiens

<400> 11

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His Glu Ala Ala Asn Gly Pro Ala Pro Leu Gly Val Arg Ala Pro Pro
 1               5                  10                  15
Ala Trp Arg Thr Ser Pro Ala Ala Glu Met Gly Ala Thr Gly Ala Ala
            20                  25                  30
Glu Pro Leu Gln Ser Val Leu Trp Val Lys Gln Gln Arg Cys Ala Val
        35                  40                  45
Ser Leu Glu Pro Ala Arg Ala Leu Leu Arg Trp Trp Arg Ser Pro Gly
    50                  55                  60
Pro Gly Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser
65                  70                  75                  80
Glu Ile Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly
                85                  90                  95
Ser Gly Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His
            100                 105                 110
Cys Val Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr
        115                 120                 125
Phe Trp Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu
    130                 135                 140
Arg Glu Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val
145                 150                 155                 160
Phe Ile Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu
                165                 170                 175
Arg Lys Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile
            180                 185                 190
Ile Val Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile
        195                 200                 205
Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly Met
    210                 215                 220
Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser Ala
225                 230                 235                 240
Gly Val Asp Gln Asn His Pro Arg Ala Val Leu Val Pro Ser Ser Leu
                245                 250                 255
Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp Cys Val Cys Tyr Ser
            260                 265                 270
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Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala Leu His Ile Val Val
        275                 280                 285
Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val His His Asn Ser Thr
    290                 295                 300
Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr Gly Phe Tyr Gly Asp
305                 310                 315                 320
Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu Gly Leu Ala Arg Tyr
                325                 330                 335
Asp Phe Ser Gly Leu Lys Thr Phe Leu Ser His His Cys Tyr Glu Gly
            340                 345                 350
Thr Val Ser Phe Leu Pro Ala Gln His Thr Val Gly Ser Pro Arg Asp
        355                 360                 365
Arg Lys Pro Cys Arg Ala Gly Cys Phe Val Cys Arg Gln Ser Lys Gln
    370                 375                 380
Gln Leu Glu Glu Glu Gln Lys Lys Ala Leu Tyr Gly Leu Glu Ala Ala
385                 390                 395                 400
Glu Asp Val Glu Glu Trp Gln Val Val Cys Gly Lys Phe Leu Ala Ile
                405                 410                 415
Asn Ala Thr Asn Met Ser Cys Ala Cys Arg Arg Ser Pro Arg Gly Leu
            420                 425                 430
Ser Pro Ala Ala His Leu Gly Asp Gly Ser Ser Asp Leu Ile Leu Ile
        435                 440                 445
Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu Ile Arg His Thr
    450                 455                 460
Asn Gln Gln Asp Gln Phe Asp Phe Thr Phe Val Glu Val Tyr Arg Val
465                 470                 475                 480
Lys Lys Phe Gln Phe Thr Ser Lys His Met Glu Asp Glu Asp Ser Asp
                485                 490                 495
Leu Lys Glu Gly Gly Lys Lys Arg Phe Gly His Ile Cys Ser Ser His
            500                 505                 510
Pro Ser Cys Cys Cys Thr Val Ser Asn Ser Ser Trp Asn Cys Asp Gly
        515                 520                 525
Glu Val Leu His Ser Pro Ala Ile Glu Val Arg Val His Cys Gln Leu
    530                 535                 540
Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Asn Pro Lys Pro Asp Ser
545                 550                 555                 560
His Ser
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<210> 12
<211> 24
<212> DNA
<213> Homo sapiens

<400> 12
cgctgcatat cgttgttggg gact 24

<210> 13
<211> 24
<212> DNA

<213> Homo sapiens

<220>
<223> random oligonucleotide

<400> 13
cgctgcatat cgttgttggg gact 24

<210> 14
<211> 24
<212> DNA
<213> Homo sapiens

<400> 14
tggtttcgta aatgaccata aata 24

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> random oligonucleotide

<400> 15
tcaactgact agatgtacat ggac 24

<210> 16
<211> 4413
<212> DNA
<213> Homo sapiens

<400> 16
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agcccggcgg cggagatggg ggcgacgggg gcggcggagc cgctgcaatc cgtgctgtgg 120
gtgaagcagc agcgctgcgc cgtgagcctg gagcccgcgc gggctctgct gcgctggtgg 180
cggagcccgg ggcccggagc cggcgccccc ggcgcggatg cctgctctgt gcctgtatct 240
gagatcatcg ccgttgagga aacagacgtt cacgggaaac atcaaggcag tggaaaatgg 300
cagaaaatgg aaaagcctta cgcttttaca gttcactgtg taaagagagc acgacggcac 360
cgctggaagt gggcgcaggt gactttctgg tgtccagagg agcagctgtg tcacttgtgg 420
ctgcagaccc tgcgggagat gctggagaag ctgacgtcca gaccaaagca tttactggta 480
tttatcaacc cgtttggagg aaaaggacaa ggcaagcgga tatatgaaag aaaagtggca 540
ccactgttca ccttagcctc catcaccact gacatcatcg ttactgaaca tgctaatcag 600
gccaaggaga ctctgtatga gattaacata gacaaatacg acggcatcgt ctgtgtcggc 660
ggagatggta tgttcagcga ggtgctgcac ggtctgattg ggaggacgca gaggagcgcc 720
ggggtcgacc agaaccaccc ccgggctgtg ctggtcccca gtagcctccg gattggaatc 780
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cacaacagca cactccttcg ctactccgtg tccctgctgg gctacggctt ctacggggac 960
atcatcaagg acagtgagaa gaaacggtgg ttgggtcttg ccagatacga cttttcaggt 1020

ttaaagacct tcctctccca ccactgctat gaagggacag tgtccttcct ccctgcacaa 1080
cacacggtgg gatctccaag ggataggaag ccctgccggg caggatgctt tgtttgcagg 1140
caaagcaagc agcagctgga ggaggagcag aagaaagcac tgtatggttt ggaagctgcg 1200
gaggacgtgg aggagtggca agtcgtctgt gggaagtttc tggccatcaa tgccacaaac 1260
atgtcctgtg cttgtcgccg gagccccagg ggcctctccc cggctgccca cttgggagac 1320
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aagaaattcc agtttacgtc gaagcacatg gaggatgagg acagcgacct caaggagggg 1500
gggaagaagc gctttgggca catttgcagc agccaccct cctgctgctg caccgtctcc 1560
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cactgccagc tggttcgact ctttgcacga ggaattgaag agaatccgaa gccagactca 1680
cacagctgag aagccggcgt cctgctctcg aactgggaaa gtgtgaaaac tatttaagat 1740
aattattaca gaccaattat gttgatatat acatttaaat gtagaaattt atttttgata 1800
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ttttcagttc tgtacgcatc tgcgggttgc agcccacgcc gcttactctc agcggatgca 1920
gctgctcact tgggggcact ggcctcttag gttttaacga tgtcaacagt gtagtttaga 1980
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tcatgtttaa caggcagcat ccattttcag aatttcctgg cattgattta tattttgaag 3060
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ttcaataaga aacccagcca ttccgcatgg ctggttcctg agtggctctg gtgatactct 3900
ccagccacct gctgacattg agaatctcag acctcgggac tgctgttgcg gtaccgtgtg 3960
tctgacacct gccagcagcc ctttgctatc tgcgcgcagg atgggggtga ctgcccagac 4020

```
attcccgcta gataggctct gatttccggg gcagcctttc agatgcggca gacatacaac    4080
acctgtactt tagagtttta agggaaaaaa aatcagaagt gctggttaga tagtaaaaac    4140
ttaggataac ttagaaaggc tagttttagc ttcctttgtg gctccctggt gcaaaacaat    4200
tagcagttat gcaatggacc tgattctagt ttattctaat taagaagtga ggccgagttt    4260
gacttcgttc ctgaatacaa tcttgagtaa ctgggaaagt ctgagtgaaa ggatggcctc    4320
attctctttc taatcttgct ggtttcaaga ttagaaaatg gcattatttg atctgaaatg    4380
tttgagaaga cacgaataaa gttacttggg cag                                4413
```

FIG. 1

```
Q: 1          PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
              P..LL:.:NPFGG:G . : :..V.P:.: A.:: ::I TE..N.A:E
H: 144        PPRLLLLVNPFGGRGLAWQWCKNHVLPMISEAGLSFNLIQ----------TERQNHARE

              TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA
               .:. :::.::DGIV.V.GDG:..EVL:GL:.R .: ..AV :P :GI:P.
              LVQGLSLSEWDGIVTVSGDGLLHEVLNGLLDR--------PDWEEAVKMP----VGILPC

              GSTDCVCYS---------TVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLG
              GS :.:. : .:G.. . ..:L :. G.. .:D: SV S :S. :.
              GSGNALAGAVNQHGGFEPALGLDLLLNCSLLLCRGGGHPLDLLSVTLASGSRCFSFLSVA

              YGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSP 223
              :GF..D:  .SE: R LG AR:... :  ..: H.Y.G.:S:LPA. . .SP
              WGFVSDVDIQSERFRALGSARFTLGTVLGLATLHTYRGRLSYLPATVEPASP 352
```

FIG. 2

PK**HLLVFINP FGGKGQGKRI YERKVAPLFT LASITTDIIG NKFYVNYVEV ITEHANQAKE TLYEINIDKY**
DGIVCVGGDG MFSEVLHGLI GRTQRSAGVD QNHPRAVLVP SSLRIGIIPA GSTDCVCYST VGTSDAETSA
LHIVVGDSLA MDVSSVHHNS TLLRYSVSLL GYGFYGDIIK DSEKKRWLGL ARYDFSGLKT FLSHHCYEGT
VSFLPAQHTV GSPRDRKPCR AGCFVCRQSK QQLEEEQKKA LYGLEAAEDV EEWQVVCGKF LAINATNMSC
ACRRSPRGLS PAAHLGDGSS DLILIRKCSR FNFLRFLIRH TNQQDQ